

A.

SEQ ID NO:1

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B.

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181 LGAIANQLKS KKVRSIIYIL PEFIRTLKGG FKDGSEKKL HRVREANILM LDDIGAEVVT  
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301 TPYFLSGENF RNN

Fig. 1

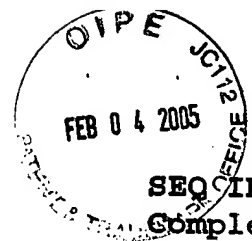


Figure 2A

SEQ ID NO : 3

Complete genome sequence of bacteriophage 77

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**Figure 2B**

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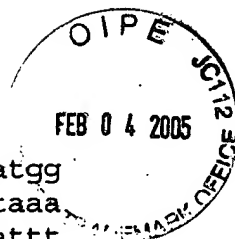


Figure 2C



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Figure 2D

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Figure 2E

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Figure 2F

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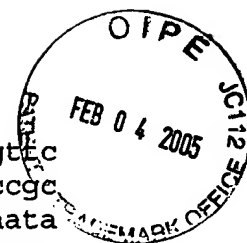


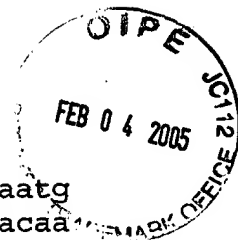
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Figure 2H

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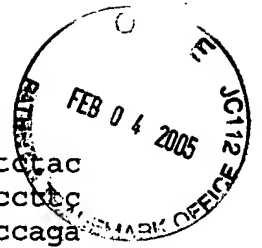


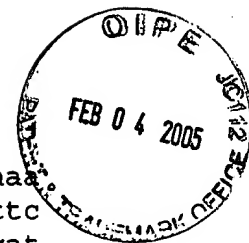
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Figure 2J

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**Figure 2K**

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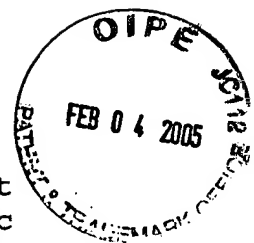


Figure 2L

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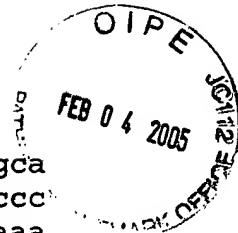


Figure 2M

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36601	tttcatccaa	atacaaataa	gtgttcgacg	tcaagtttta	ttccaattga	tatccccttc
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37321	caagaagcaa	cgagatgagc	ttattgggga	tatagcgaag	ttacgagatt	gtaacaaaga
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37441	aaacgaattc	ggtaacgatg	atgaaagagt	taaattcgga	atggaattaa	acaataaaat
37501	ttttatggag	gatgacacaa	atgaataatc	gcgaaaaaat	cgaacagtcc	gttatttagtg
37561	ctagtgcgta	taacggtaat	gacacagagg	ggttgctaaa	agagattgag	gacgtgtata
37621	agaaagcgca	agcgtttgat	gaaatacttg	agggaatgac	aatgctatt	caacattcag
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38041	aatgatgaag	aacgtgatgg	aatacccttt	ttatatgatg	atatagacgc	tgaattagaa
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38161	agaagagttt	accaaataca	caaaggcgat	aaactagctc	aattgggttat	cgtgcctata
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38401	actgtggcta	gagataatca	gacgtttaca	gttattgagg	cagagagtaa	agaagaagcg
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38641	atggttatat	ttacgcaagt	actataatca	agaaaccaac	gtatattaaa	acagatacga
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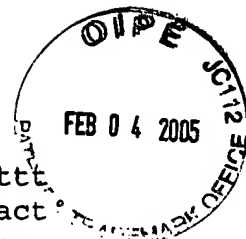
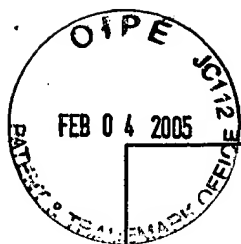


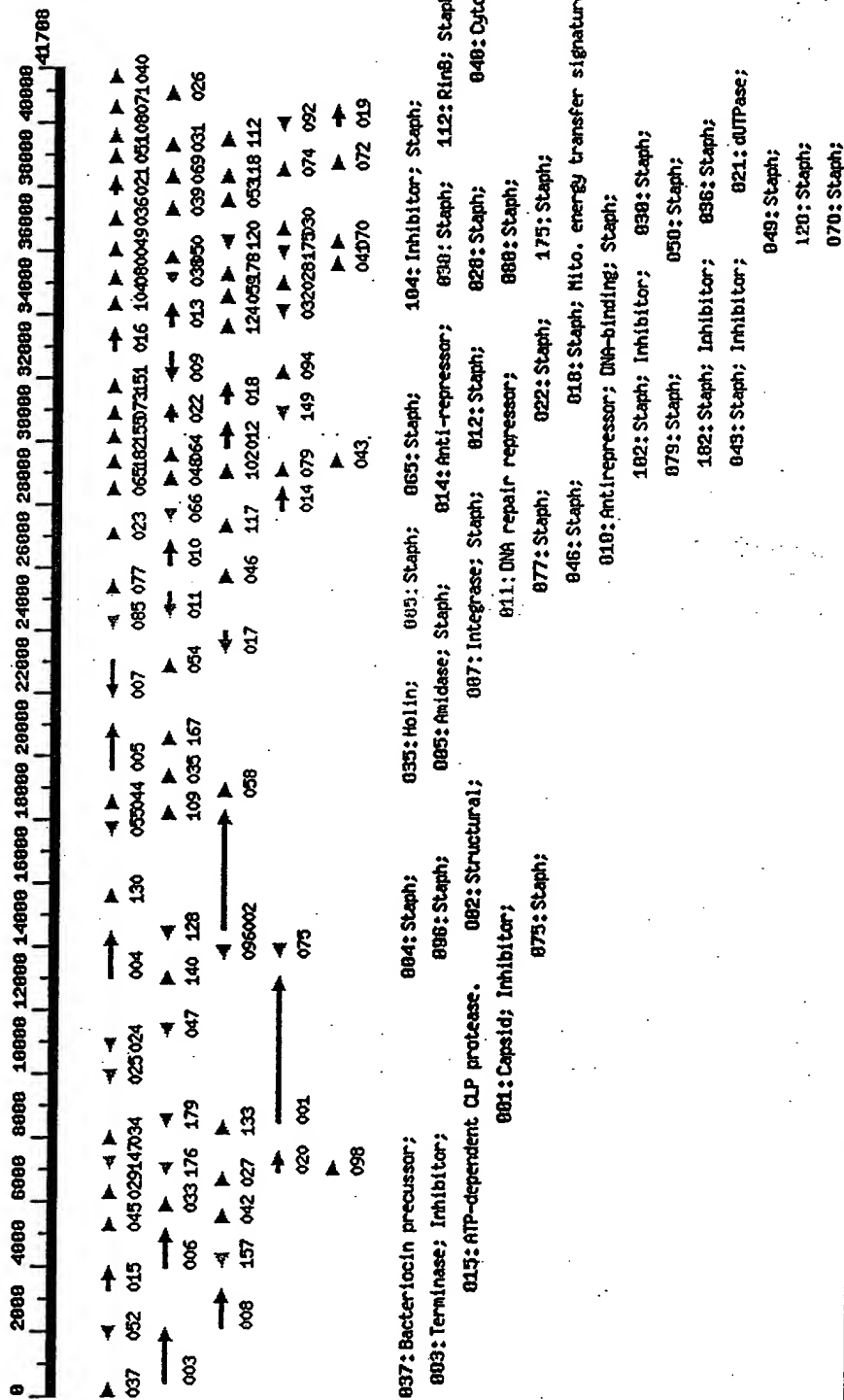
Figure 2N

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38881 tgtattgaac aaagggtata tagttgggat caatgttgag gaggcagatg atgattaaca  
38941 tacctaaaaat gaaattccccg aaaaagtaca ctgaaataat caaaaaatat aaaaataaag  
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39061 gtgaattthta cagtcctacg atggctaata tgaatgaata tgaattaagg gctatgttaa  
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39421 agcgcagata tacaagctag gttaaaagta ggcgataagg tagaagttaa aacaatcggt  
39481 tatagaatac actthtttaa tttatatccg gtcttatacg aagtaaagaa ggtagataaa  
39541 caatgattaa acaaatacta agactattat tcttactagc aatgtatgag ttaggtaagt  
39601 atgtaactga gcaagtgtat attatgatga cggctaata tgaatgtagag gcgccgagtg  
39661 attacgtctt tgcagcggag gtgagtgaat aatgagaata thttattht atthtgatcgt  
39721 thtgctgtht gctthtctaa tatccatata tattattgat gatggagtga taataaatgc  
39781 attaggaatt thtggtatgt ataaaattat agattcctth tcaaaaaa ttataaagag  
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39901 gctthattca gttaaagaga thtttaggta thttacagat tctaacttac aacgtaaaaa  
39961 aatcaattta gaacaaatat atccgatata thtagattgt thtaaaaagg ctaaaaagat  
40021 gattggagct tatattattc caacagaaca gcatgaattt ttagatttht ttgatattga  
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40381 aaacgattat aatctthtct thgataaatt tgaagaacag thtagtcaa agthtthaaat  
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40501 atgtggatta ctatgactat tgtatttgct atattgctat tagthtgtat cagtattaat  
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40621 gtagthtaaaa ctaaagggtta caacgggtta gaagaatata ggattgaatt gaagcgaatg  
40681 aataacgata thtaaaaagta atthtatatta tccggaggtat tgcattgaat gataaagatt  
40741 gagaaacacg atatcaaaaa gcttgaagaa tacattcagc acatcgataa ctatcgaaga  
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40981 gatgaggata cgcttgagth atthaaggth agatattggg atthtctctat tggthgtht  
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41101 aatgcactga tgcataagth agcaaagtat atthgthtatt tgtagcggac thttacccta  
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41341 tcttgatact actthaagth tataagggtga aacattatga tgactaaaga cgaacgtata  
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41461 tatgaatgtc aacaatgtaa gagagacggc aagthtaacga catatgacaa aagcaagcgt  
41521 aagtcgthtg atgtagatca tatattatcg ctagaacatc atccggagth tgctcatgac  
41581 thaaacaatt tagaaacact gtgtattthaa tgtcacacaa aaaaagaaaa gagattthata  
41641 aaaaagaaaa ataatggaa agacgaaaaa tggtaaatat ccccggtca aaaaatcaa  
41701 aagcgatc

Fig. 3



Phage: Bacteriophage 77  
Minimal ORF size: 33 a.a.  
ORFs "with" RBS.  
Number of ORFs: 99



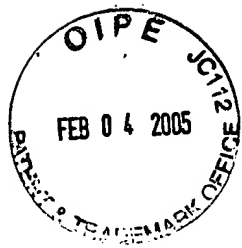


Fig. 4

P77ORF104

SEQ ID NO: 4

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61  ctcatagatg aggcacaggg cgatgaaaat aggttgtagc acctatttat ccaaaaactt
121 gcagaacgtc atacacgccc cgctatcgtc gaatattaa
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SEQ ID NO: 5

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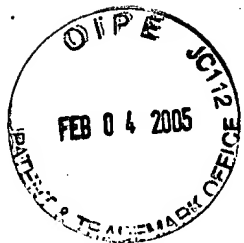


Fig. 5

**Predicted Tryptic Peptide Masses of Conceptual ORF in Contig 1383:**

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1  M G G G Q S I M K q f k S I I N T S Q D F E K r I E K j k K 30
31  e v i n d p d v k Q F L E A H R a e l t n a m i d e d i n v 60
61  l q e y k D Q Q K h y d g h k F A D C P N F V K g h v p e l 90
91  y v d n n r I K i r Y L Q C P C K i k Y D E E R t e a e l i 120
121 t s h n m q r D T L N A K i k D I Y M N H R d r L D V A M A 150
151 A D D I C T A I T N G E Q V K g l y l y g p f g t g k S F I 180
181 L G A I A N Q L K s k K v r S T I I Y L P E F I R t i k G G 210
211 F K d g s f e k K i h r V R e a n i m i d d i g a e e v t 240
241 p w v r D E V I G P L L H Y R m v h e l p t f f s s n f d y 270
271 s e l e h h l a m t r D G E E K t k A A R i e r V K s l s 300
301 t p y f l s g e n f r N N 313
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**Tryptic peptide fragment:**

**GHVPELYVDNNR**

**Predicted Peptide Mass MH+ = 1413.538**

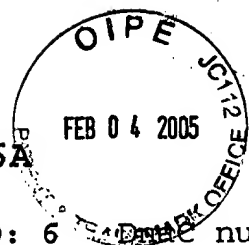
**STIIYLPEFIR**

**Predicted Peptide Mass MH+ = 1351.6221**

**SLSTPYFLSGENFR**

**Predicted Peptide Mass MH+ = 1618.7923**

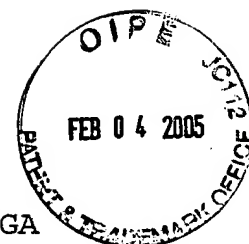
Figure 6A



SEQ ID NO: 6 nucleotide *B. subtilis*

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1   ATGACAGACC TTCTGAATGA CCGGCTTCCT CCGCAAAATA TAGAAGCCGA
51  ACAAGCCGTG TTAGGCGCTA TTTTTTTACA GCCGTCTGCT TTAACACTGG
101 C TTCAGAAAGT ATTGATTCCA GATGATTCTT ATAGAATGTC CCACCAAAAA
151 ATCTATAATG CGATGCTGGT GCTCGGTGAC CGAGGTGAAC CGGTTGATCT
201 GGTGACAGTT ACATCAGAGC TTGCGAACAC AGACCTGCTG GAAGAAGTAG
251 GCGGTATTTT ATATTTGACA GATATCGCAA ACTCGGTGCC GACAGCGGCT
301 AACATAGAAT ATTACGCGAA AATCGTTGAG GAAAAATCGA TTCTTCGCCG
351 ATTAATCAGA ACTGCGACAA CGATTGCTCA AGACGGGTAT ACCCGTGAGG
401 ATGAGGTCGA GGATTTACTC AGTGAAGCGG AAAAAACGAT TATGGAAGTG
451 GCACAGCGCA AAAACACGAG TGCCTTCCAA AATATTAAGG ACGTCCTTGT
501 CCAGACCTAT GATAATATCG AACAGCTTTA CAATCGAAAA GGTGATATCA
551 CGGGAATTCC AACAGGGTTT ACGGAGCTTG ACCGGATGAC TGCGGGTTTC
601 CAGCGCAACG ACTTGATCAT TGTGGCTGCC CGTCCTTCAG TAGGGAAAAC
651 AGCCTTTGCC CTGAACATCG CACAAAACGT GCGGACGAAG ACCGATGAGA
701 GCGTAGCGAT TTTCAGTCTT GAGATGGGTG CCGAGCAGCT CGTTATGCGT
751 ATGCTCTGTG CCGAGGGAAA TATCAATGCC CAGAATCTCC GTACAGGTAA
801 CCTGACCGAA GAGGATTGGG GCAAGCTGAC GATGGCAATG GGAAGCCTAT
851 CGAACAGCGG GATTTACATC GATGATACAC CGGGTATTTC AGTGAGTGAA
901 ATCCGTGCCA AGTGCCGCCG CTTGAAGCAG GAAAGCGGGC TGGGCATGAT
951 TTTGATCGAT TACCTGCAAT TGATTCAGGG AAGCGGTCGT TCAAAGGACA
1001 ACCGTCAGCA GGAAGTATCT GAAATTTCCC GTGAACTGAA GTCGATTGCG
1051 AGGGAGCTGC AAGTCCCTGT TATCGCGCTT TCTCAGCTTT CCAGGGGTGT
1101 TGAGCAGCGT CAGGATAAAC GTCCGATGAT GTCTGATATC CGGGAATCAG
1151 GAAGTATCGA GCAGGACGCG GATATTGTCG CGTTCCTTTA TCGTGATGAC
1201 TACTATGACA AAGAAACCGA GAATAAAAAT ATTATCGAAA TTATTATCGC
1251 CAAACAGCGT AACGGCCCGG TAGGAACCGT GTCTCTTGCG TTCGTAAAAG
1301 AATACAACAA ATTCGTCAAC CTGGAACGGC GTTTTGATGA CGCAGGCGTT
1351 CCGCCCGGCG CA
```

Figure 6B



SEQ ID NO: 7 DnaC nucleotide *S. aureus*

```
1  ATGGATAGAA TGTATGAGCA AAATCAAATG CCGCATAACA ATGAAGCTGA
51  ACAGTCTGTC TTAGGTTCAA TTATTATAGA TCCAGAATTG ATTAATACTA
101 CTCAGGAAGT TTTGCTTCCT GAGTCGTTTT ATAGGGGTGC CCATCAACAT
151 ATTTTCCGTG CAATGATGCA CTTAAATGAA GATAATAAAG AAATTGATGT
201 TGTAACATTG ATGGATCAAT TATCGACGGA AGGTACGTTG AATGAAGCGG
251 GTGGCCCGCA ATATCTTGCA GAGTTATCTA CAAATGTACC AACGACGCGA
301 AATGTTTCAGT ATTATACTGA TATCGTTTCT AAGCATGCAT TAAAACGTAG
351 ATTGATTCAA ACTGCAGATA GTATTGCCAA TGATGGATAT AATGATGAAC
401 TTGAACTAGA TGCGATTTTA AGTGATGCAG AACGTCGAAT TTTAGAGCTA
451 TCATCTTCTC GTGAAAGCGA TGGCTTTAAA GACATTCGAG ACGTCTTAGG
501 ACAAGTGTAT GAAACAGCTG AAGAGCTTGA TCAAAATAGT GGTCAAACAC
551 CAGGTATACC TACAGGATAT CGAGATTTAG ACCAAATGAC AGCAGGGTTC
601 AACCAGAAATG ATTTAATTAT CCTTGCAGCG CGTCCATCTG TAGGTAAGAC
651 TCGTTCGCA CTTAATATTG CACAAAAGT TGCAACGCAT GAAGATATGT
701 ATACAGTTGG TATTTTCTCG CTAGAGATGG GTGCTGATCA GTTAGCCACA
751 CGTATGATTG TAGTTCTGG AAATGTTGAC TCAAACCGCT TAAGAACGGG
801 TACTATGACT GAGGAAGATT GGAGTCGTTT TACTATAGCG GTAGGTAAAT
851 TATCACGTAC GAAGATTTTT ATTGATGATA CACCGGGTAT TCGAATTAAT
901 GATTTACGTT CTAAATGTCG TCGATTAAAG CAAGAACATG GCTTAGACAT
951 GATTGTGATT GACTACTTAC AGTTGATTCA AGGTAGTGGT TCACGTGCGT
1001 CCGATAACAG ACAACAGGAA GTTTCTGAAA TCTCTCGTAC ATTAAAAGCA
1051 TTAGCCCGTG AATTAGAATG TCCAGTTATC GCATTAAGTC AGTTATCTCG
1101 TGGTGTTGAA CAACGACAAG ATAAACGTCC AATGATGAGT GATATTCGTG
1151 AATCTGGTTC GATTGAGCAA GATGCCGATA TCGTTGCATT CTTATACCGT
1201 GATGATTACT ATAACCGTGG CGGCGATGAA GATGATGACG ATGATGGTGG
1251 TTTCGAGCCA CAAACGAATG ATGAAAACGG TGAAATTGAA ATTATCATTG
1301 CTAAGCAACG TAACGGTCCA ACAGGCACAG TTAAGTTACA TTTTATGAAA
1351 CAATATAATA AATTTACCGA TATCGATTAT GCACATGCAG ATATGATGTA
1401 A
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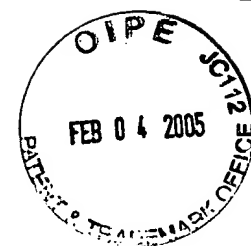


Figure 6C

Optimal global alignment

Sequence 1 SEQ ID NO: 6 DnaC nucleotide *B. subtilis*(1471 letters)

Sequence 2 SEQ ID NO: 7 DnaC nucleotide *S. aureus*(1513 letters)

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seq1      1 AT-GACAGACCTTCTGAATGACCGGCTTC---CTCCGCAAAATATAGAAGCCGAACAAGC      56
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seq2      1 ATGGATAGA---ATGTATGAGCAAAATCAAATGCCGCATAACAATGAAGCTGAACAGTC      56

seq1     57 CGTGTTAGGCGCTATTTTTTTTACAGCC-GTCTGCTTTAACTGCTTCAGAAGTATTGA      115
          || || || || || || || || || || || || || || || || || || || || ||
seq2     57 TGTCTTAGGTTCAATTATTATAGATCCAGAATTGATTAATACT-ACTCAGGAAGTTTTCG      115

seq1    116 TTCCAGATGATTTCTATAGAATGTCCACCAAAAAATCTATAATGCGATGCTGGTGCTCG      175
          || || || || || || || || || || || || || || || || || || || || ||
seq2    116 TTCCTGAGTCGTTTTATAGGGGTGCCCATCAACATATTTTCCGTGCAATGATGCACCTAA      175

seq1    176 GTGACCGAGGTGAACCGGTTGATCTGGTGACA--GTTACATCAGAGCTTGCGAACACAGA      233
          || || || || || || || || || || || || || || || || || || || || ||
seq2    176 ATGAAGATAATAAAGAAATTGATGTTGTAACATTGATGGATC--AATTATCGACGGAAGG      233

seq1    234 CCTGCTGGAAGAAGTAGGCGGTATTTTCATAT-TTG-ACAGATATCGCAAACTCGGTGCCG      291
          || || || || || || || || || || || || || || || || || || || || ||
seq2    234 TACGTTGAATGAAGCGGTGGCCCGCAATATCTTGACAGATTATCTACAAAT--GTACCA      291

seq1    292 ACAGCGGCTAACATAGAAATATTACGCGAAAATCGTTGAGGAAAAATCGATT-CTTCGCCG      350
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seq2    292 ACGACGCGAAATGTTTCAGTATTATACTGATATCGTT-TCTAAGCATGCATTAAACGCTAG      350

seq1    351 ATTAATCAGAACTGCGACAACGATTGCTCAAGACGGGTATACCCGTGAGGATGAGGTCTGA      410
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seq2    351 ATTGATTCAAACCTGCAGATAGTATTGCCAATGATGGATATAATGATGAACCTGAACTAGA      410

seq1    411 --GGATTTACTCAGTGAAGCGGAAAAAACGATTATGGAAGTGGCA-CAGCGCAAAAACAC      467
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seq1    468 GAGTGCCTTCCAAAATATTAAGGACGTCCTTGTCAGACCTATGATAATATC-GAACAGC      526
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seq1    527 TTTACAATCGAAAAAGGTGAT--ATCA-CGGGAATTCCAACAGGGTTTACGGAGCTTGACC      583
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seq2    584 AAATGACAGCAGGGTTCAACCGAAATGATTTAATTATCCTTGACGCGCGTCCATCTGTAG      643

seq1    644 GGAAAACAGCCTTTGCCCTGAACATCGCACAAAACGTGGCGAC----GAAGACCGATG-A      698
          || || || || || || || || || || || || || || || || || || || || ||
seq2    644 GTAAGACTGCGTTTCGCACTTAATATTGCACAAAAGTTGCAACGCATGAAGA--TATGTA      701
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seq1	699	GAGCGTAGCGATTTTTCAGTCTTGAGATGGGTGCCGAGCAGCTCGTTATGCGTATGCTCTG	
seq2	702	TACAGTTGGTATTTTCTCGCTAGAGATGGGTGCTGATCAGTTAGCCACACGTATGATTTG	761
seq1	759	TGCCGAGGGAAATATCAATGCCCAGAATC---TCCGTACAGGTAACCTGACCGAAGAGGA	815
seq2	762	TAGTTCTGGAAATGT---TGA CTCAAACCGCTTAAGAACGGGTACTATGACTGAGGAAGA	818
seq1	816	TTGGGGCAAGCTGACGATGGCAATGGGAAGCCTATCGAACAGCGGGATTACATCGATGA	875
seq2	819	TTGGAGTCGTTTTACTATAGCGGTAGGTAAATTATCACGTACGAAGATTTTTATTGATGA	878
seq1	876	TACACCGGGTATTTCGAGTGAGTGAAATCCGTGCCAAGTGCCGCCGCTTGAAGCAGGAAAG	935
seq2	879	TACACCGGGTATTTCGAATTAATGATTTACGTTCTAAATGTCGTCGATTAAAGCAAGAACA	938
seq1	936	CGGGCTGGGCATGATTTTGATCGATTACCTGCAATTGATTACAGGGAAGCGGT---CGTTC	992
seq2	939	TGGCTTAGACATGATTGTGATTGACTACTTACAGTTGATTCAAGGTAGTGGTTCACGTGC	998
seq1	993	AAAGGACAACCGTCAGCAGGAAGTATCTGAAATTTCCCGTGAAGTGAAGTCGATTGCGAG	1052
seq2	999	GTCCGATAACAGACAACAGGAAGTTTCTGAAATCTCTCGTACATTAAAAGCATTAGCCCCG	1058
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seq2	1059	TGAATTAGAATGTCCAGTTATCGCATTAAGTCAGTTATCTCGTGGTGTGTAACAACGACA	1118
seq1	1113	GGATAAACGTCCGATGATGTCTGATATCCGGGAATCAGGAAGTATCGAGCAGGACGCGGA	1172
seq2	1119	AGATAAACGTCCAATGATGAGTGATATTCTGTGAATCTGGTTCGATTGAGCAAGATGCCGA	1178
seq1	1173	TATTGTCGCGTTCCTTTTATCGTGATGACTACT-----ATGA	1208
seq2	1179	TATCGTTGCATTCTTATACCGTGATGATTACTATAACCGTGGCGGCGATGAAGATGATGA	1238
seq1	1209	CAAAGA-----AACCGA--GAATAAAA--ATATTATCGAAATTATTAT	1247
seq2	1239	CGATGATGGTGGTFTTCGAGCCACAAACGAATGATGAAAACGGTGAAATTGAAATTATCAT	1298
seq1	1248	CGCCAAACAGCGTAACGGCCCGGTAGGAACCGTGTCCTTGC-GTTCGTAAAAGAATACA	1306
seq2	1299	TGCTAAGCAACGTAAACGGTCCAACAGGCACAGT-TAAGTTACATTTTATGAAACAATATA	1357
seq1	1307	ACAAATTTCGTCAACCTGGAACGGCGTTTTTGATGACGCAGGCGTTCGCCCGGCGCA	1362
seq2	1358	ATAAATT---TACCGATATCG--ATTATGCACATGCAGATATGATG-----TAA	1401

FEB 04 2005

Figure 6D

SEQ ID NO: 8 DnaC *B. subtilis*

```

1   MTDLLNDRLP PQNIEAEQAV LGAIFLQPSA LTLASEVLIP DDFYRMSHQK
51  IYNAMLVLGD RGEVVDLVTV TSELANTDLL EEVGGISYLT DIANSVPTAA
101 NIEYYAKIVE EKSILRRLIR TATTIAQDGY TREDEVEDLL SEAEKTIMEV
151 AQRKNTSAFQ NIKDVLVQTY DNIEQLYNRK GDITGIPTGF TELDRMTAGF
201 QRNDLIIVAA RPSVGKTAFV LNIAQNVATK TDESVAIFSL EMGAEQLVMR
251 MLCAEGNINA QNLRTGNLTE EDWGKLTAM GSLSNSGIYI DDTPGIRVSE
301 IRAKCRRLKQ ESGLGMLID YLQLIQSGSR SKDNRQQEVS EISRELKSIA
351 RELQVPVIAL SQLSRGVEQR QDKRPMMSDI RESGSIEQDA DIVAFLYRDD
401 YYDKETENKN IIEIIIAKQR NGPVGTVSLA FVKEYNKFVN LERRFDDAGV
451 PPGA

```

SEQ ID NO: 9 DnaC *S. aureus*

```

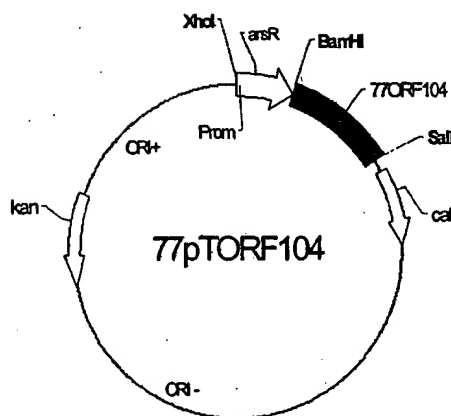
1   MDRMYEQNQ M PHNNEAEQSV LGSIIIDPEL INTTQEVLLP ESFYRGAHQH
51  IFRAMMHLNE DNKEIDVVTI MDQLSTEGTL NEAGGPQYLA ELSTNVPTTR
101 NVQYYTDIVS KHALKRRLIQ TADSIANDGY NDELELDAIL SDAERRILEL
151 SSSRES DGFK DIRDLVGQVY ETAEELDQNS GQTPGIPTGY RDLDQMTAGF
201 NRNDLIILAA RPSVGKTAFV LNIAQKVATH EDMYTVGIFS LEMGADQLAT
251 RMICSSGNVD SNRLRTGTMT EEDWSRFTIA VGKLSRTKIF IDDTPGIRIN
301 DLRSKCRRLK QEHGLDMIVI DYQLIQSGSG SRASDNRQQE VSEISRTLKA
351 LARELECPVI ALSQLSRGVE QRQDKRPMMS DIRESGSIEQ DADIVAFLYR
401 DDYYNRGGDE DDDDDGGFEP QTNDENGEIE IIIAKQRNGP TGTVKLHFMK
451 QYNKFTDIDY AHADMM

```

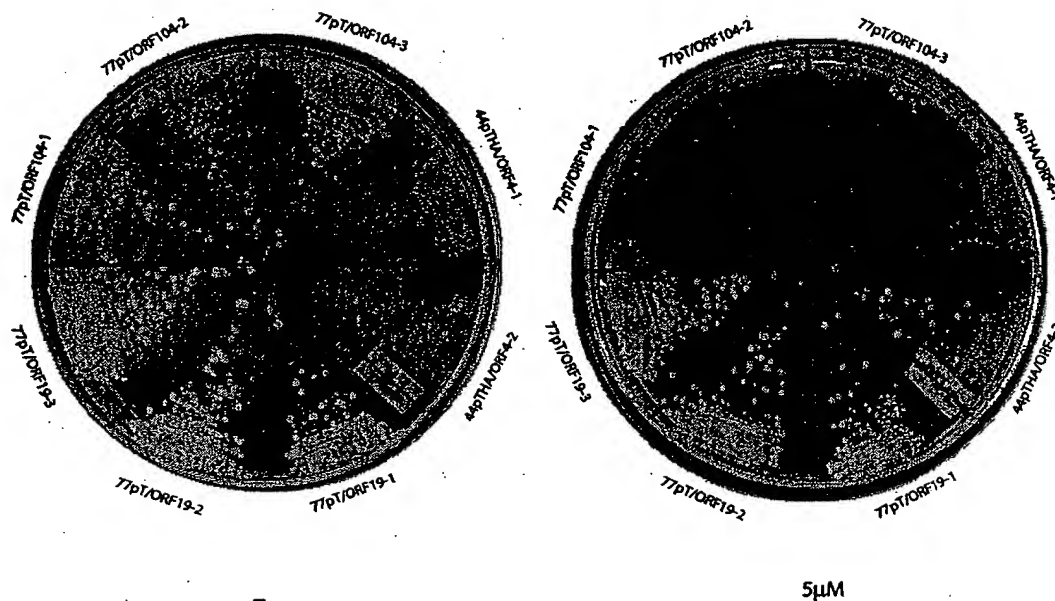


FIGURE 7

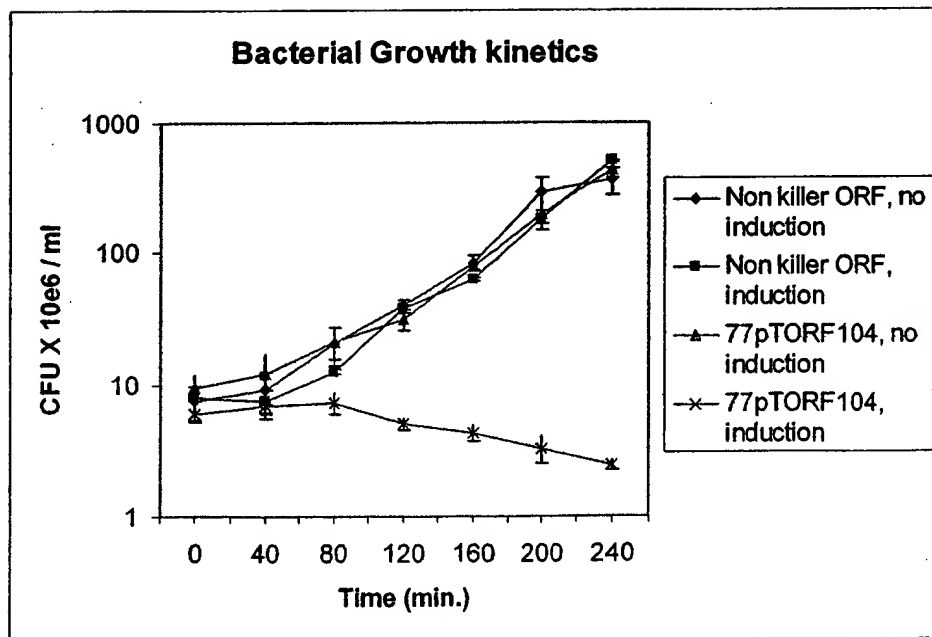
7A-



7B-



7C-





GST

GST/ORF104

ACB 0 0.1 0.5 1.0 2.0    ACB 0 0.1 0.5 1.0 2.0    Mr

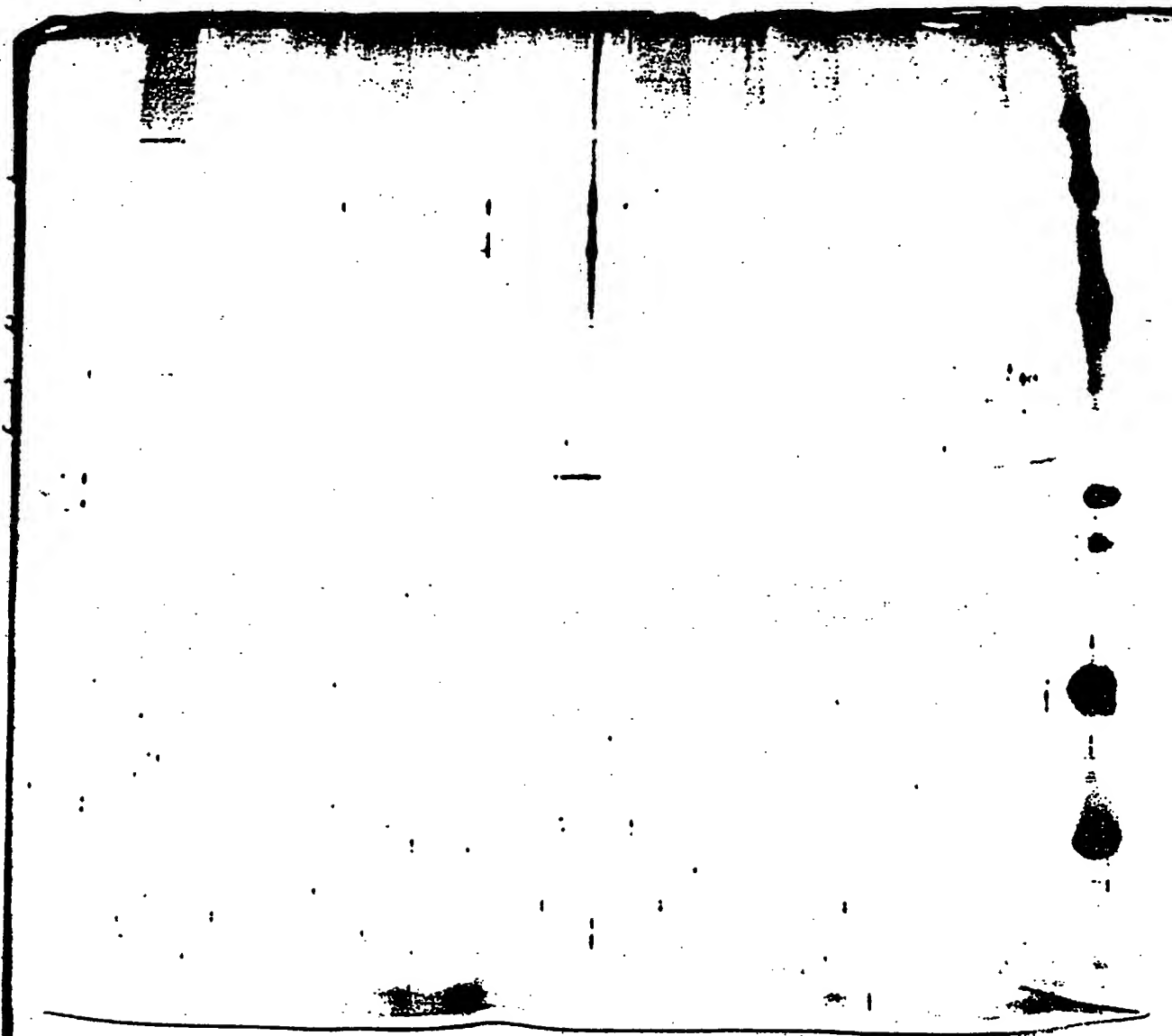
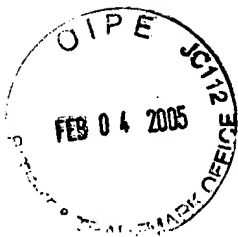


Fig. 8 A



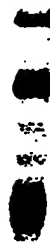


GST

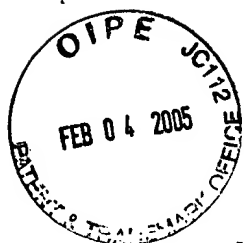
GST/ORF104

ACB 0 0.1 0.5 1.0 2.0 Mr

ACB 0 0.1 0.5 1.0 2.0



83



GST

GST/ ORF104

Mr ACB 0 0.1 0.5 1.0 2.0

ACB 0 0.1 0.5 1.0 2.0

97

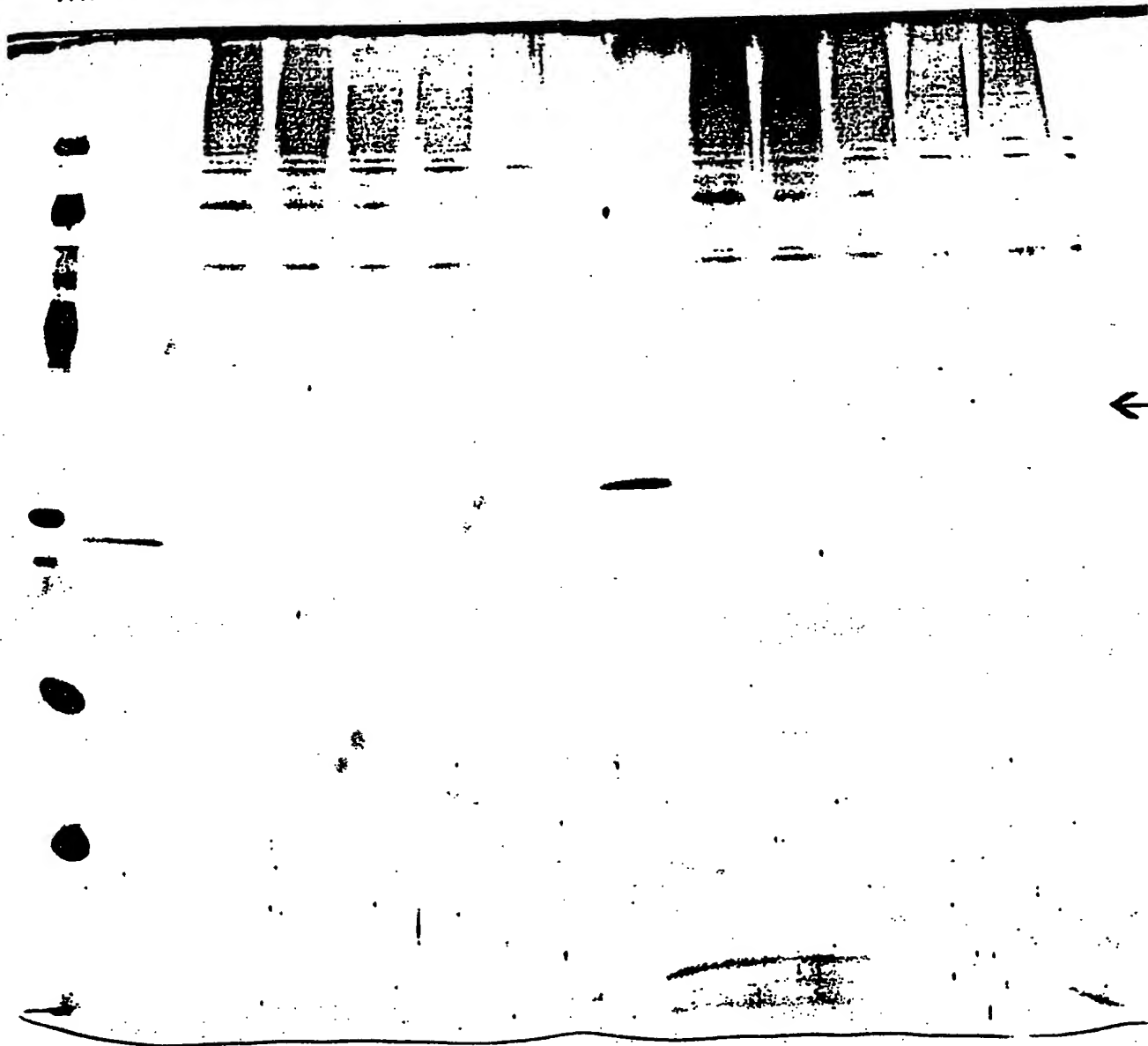
66

45

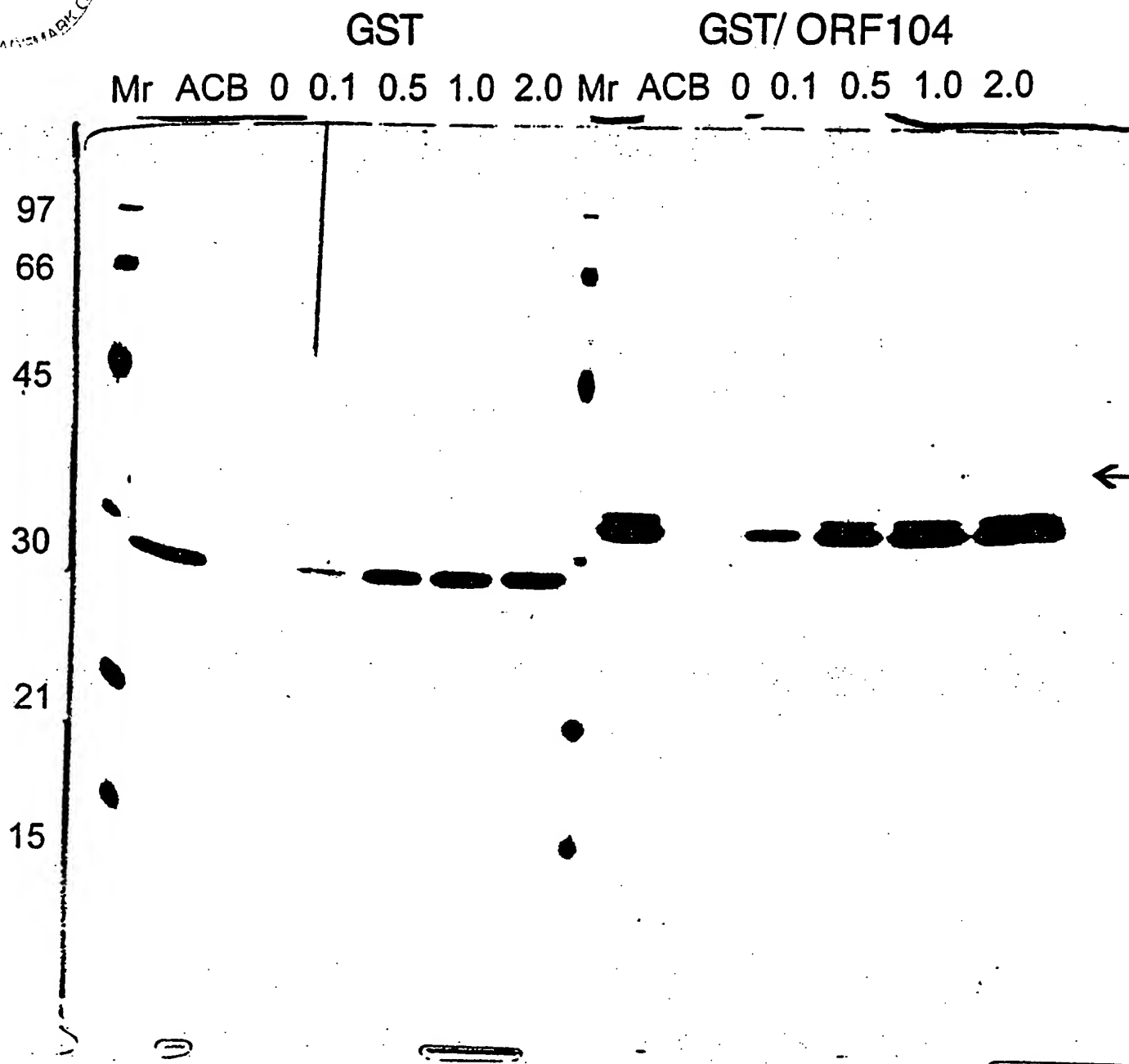
30

21

15



8C



SD

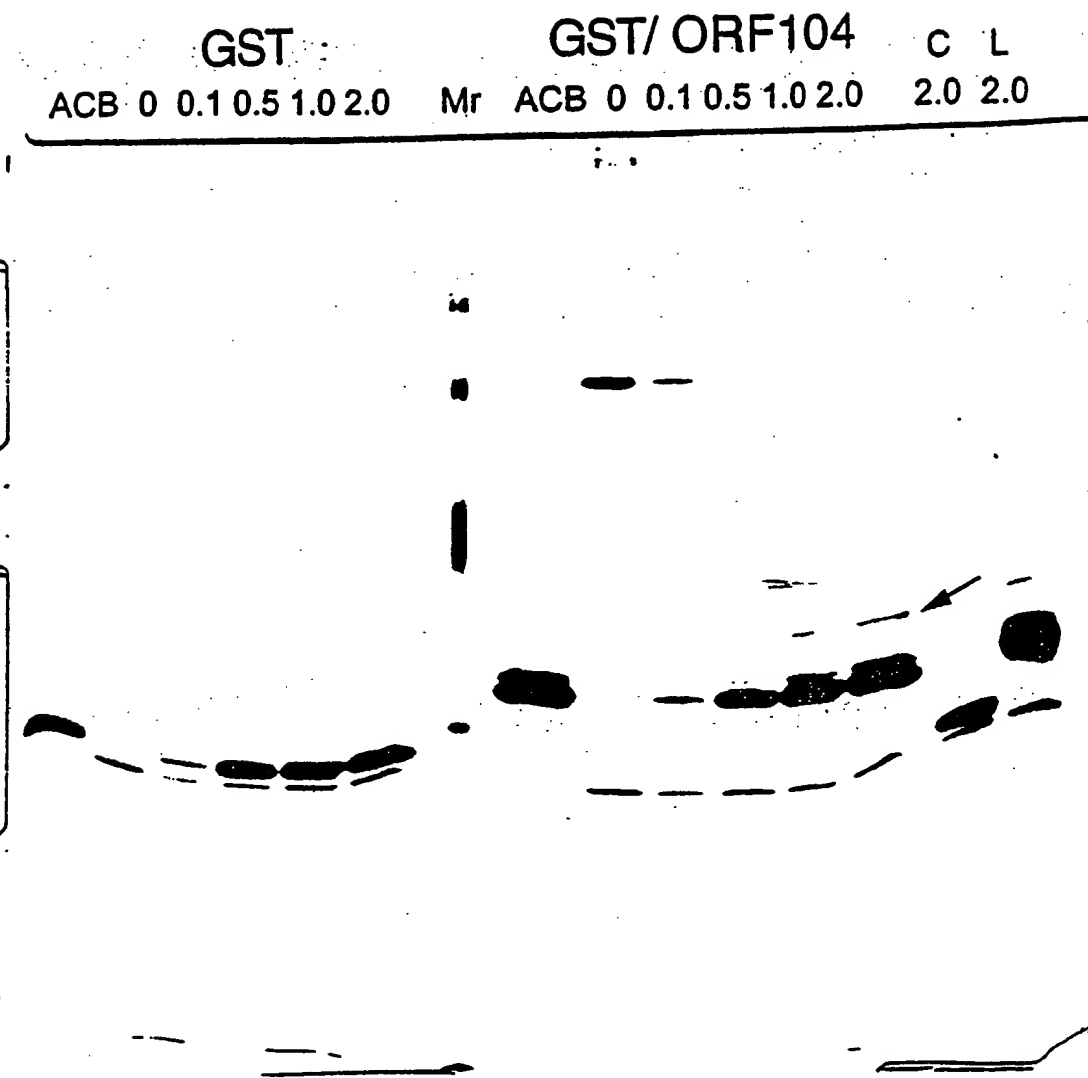
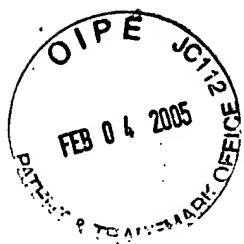


Fig. 9



Lys Extract                      FP/S Extract  
ACB 0 0.1 0.5 1.0 2.0    Mr    ACB 0 0.1 0.5 1.0 2.0

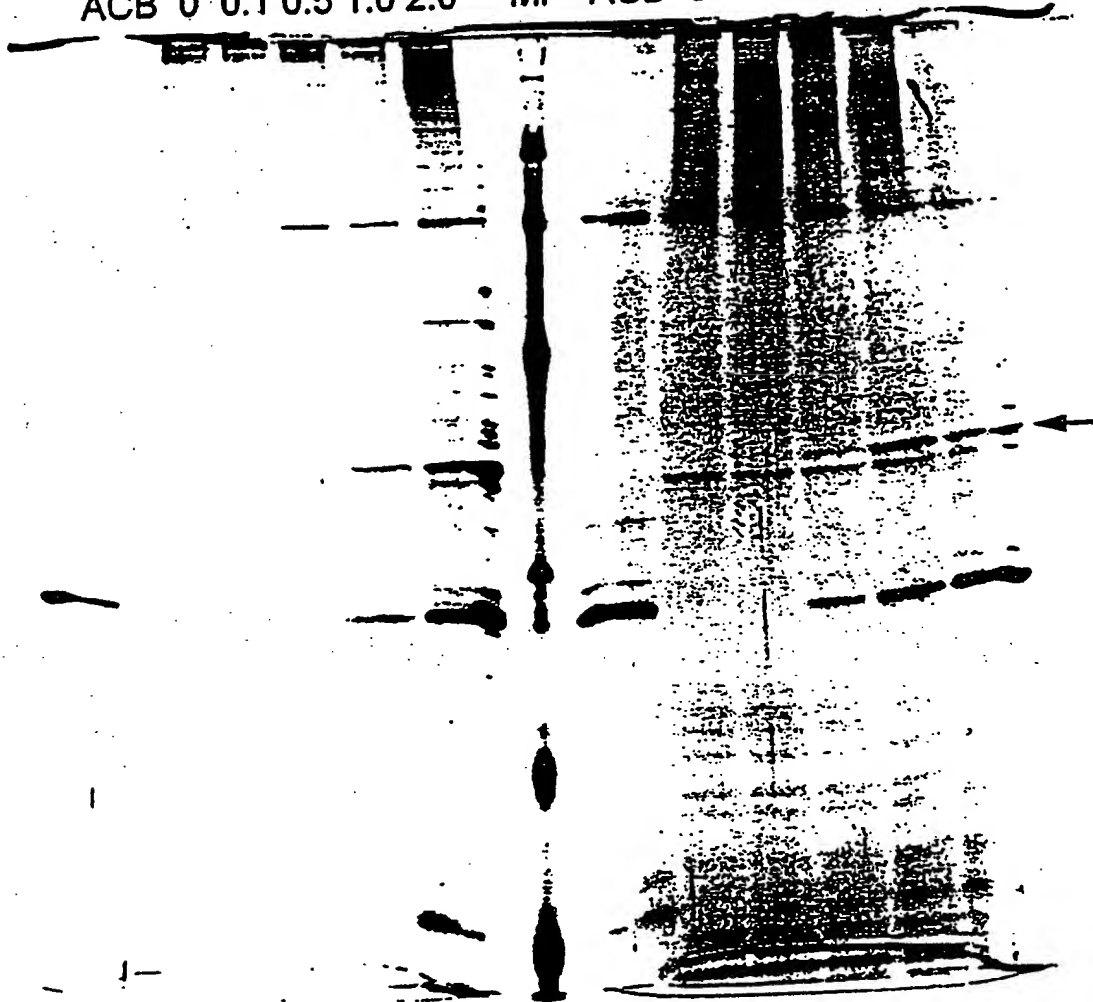
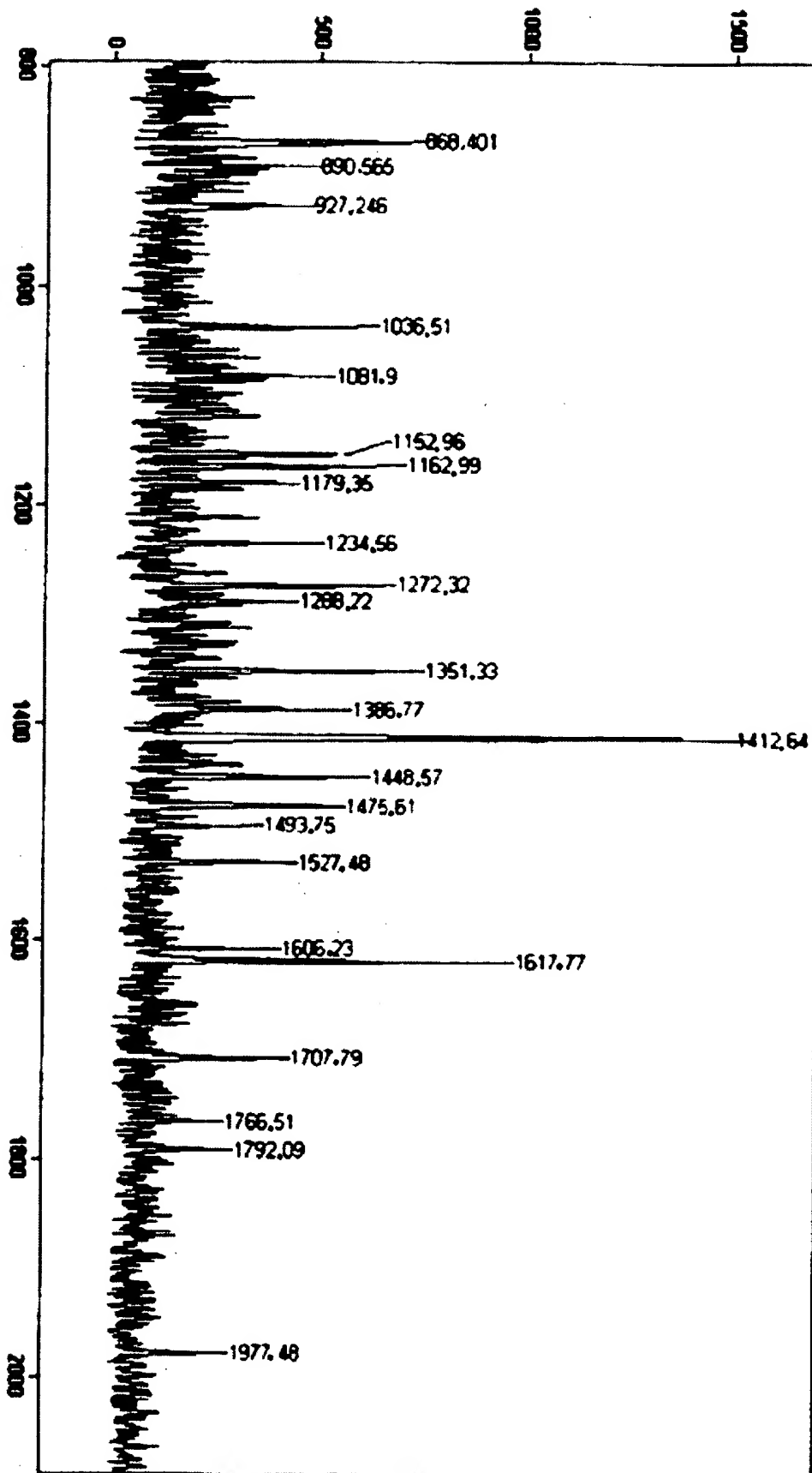


Fig. 10



**Figure 11A:**

i) Tryptic peptide mass spectrum of interacting protein (1% Triton X-100 elute)







**Figure 11B:**  
ii) Tryptic peptide mass spectrum of interacting protein (1% SDS eluate)

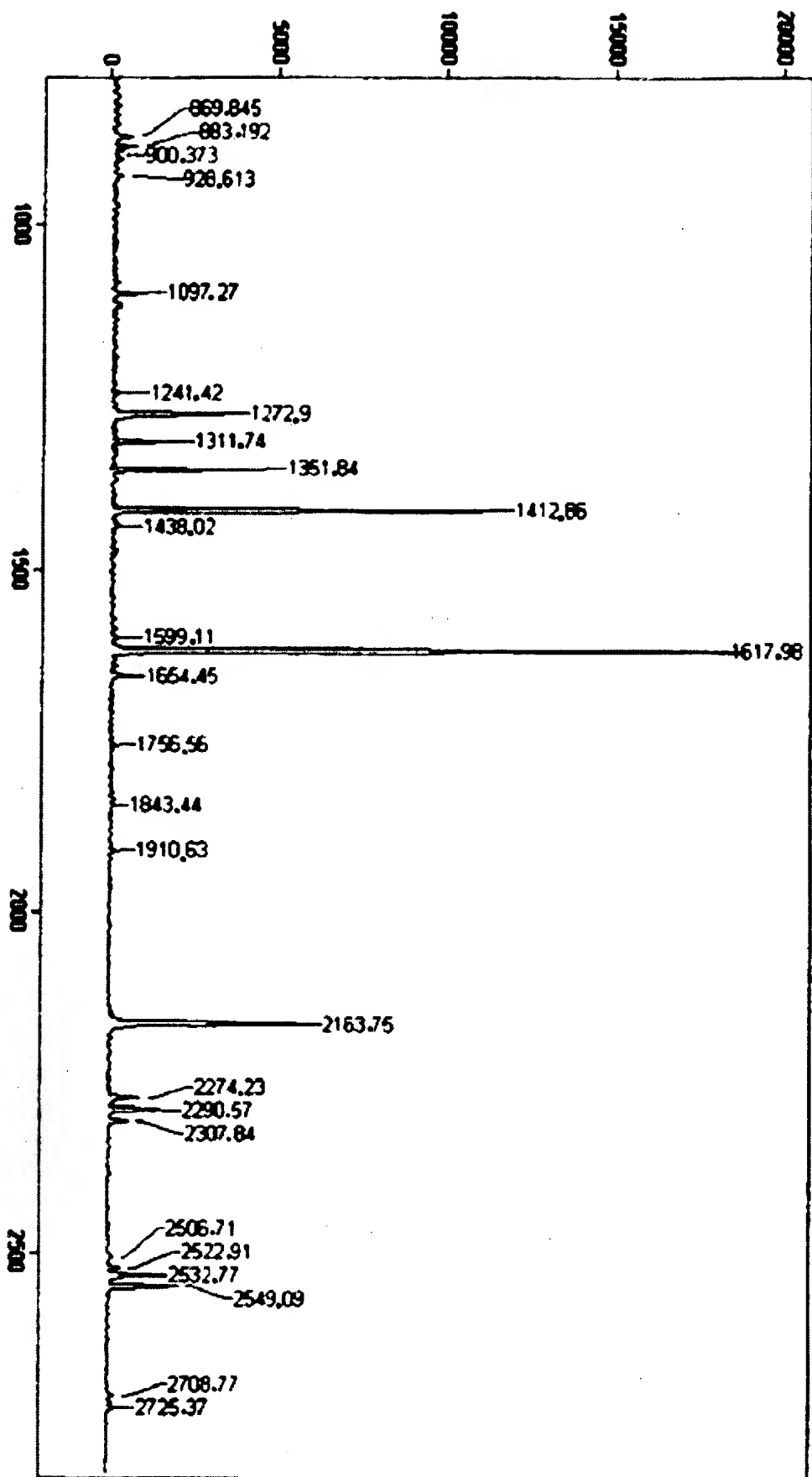
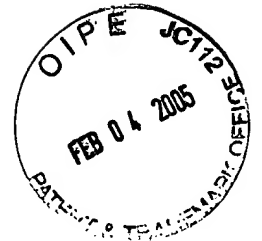
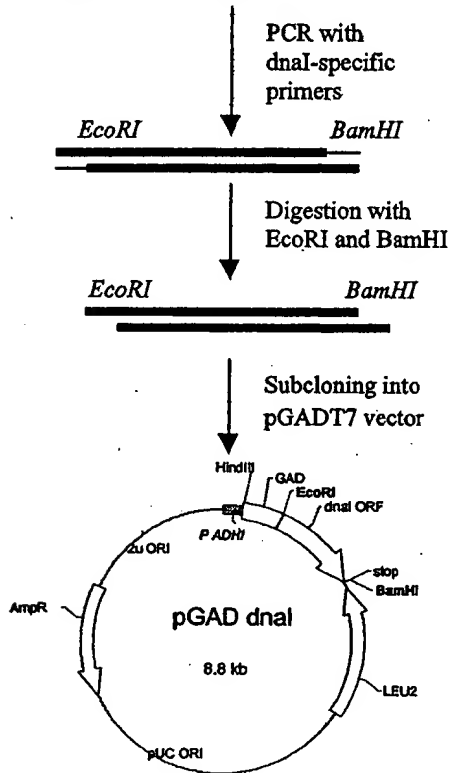


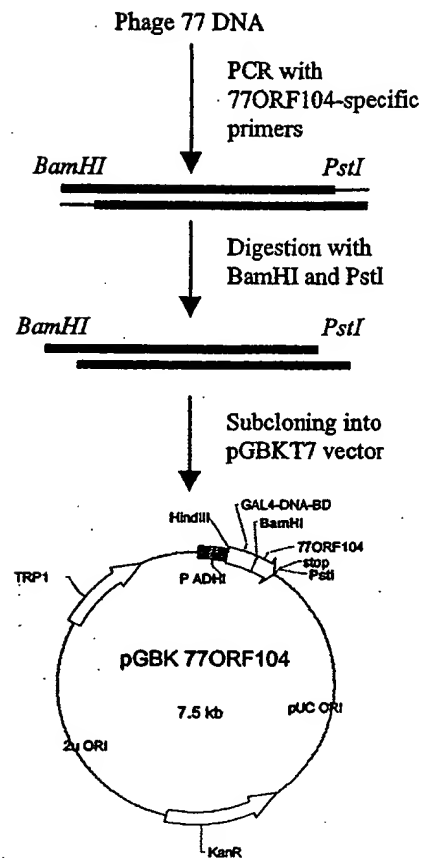
Figure 12



A- *Staphylococcus aureus* genomic DNA



B-



C-

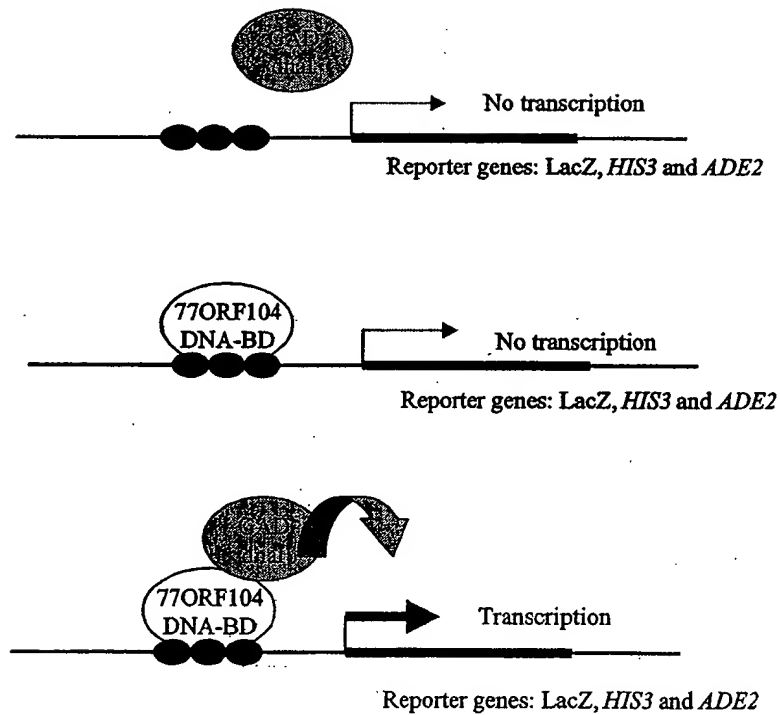
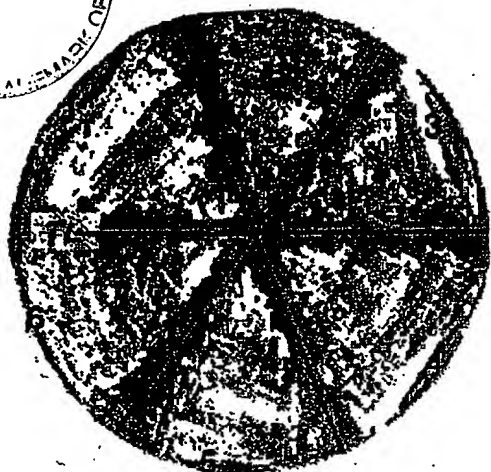
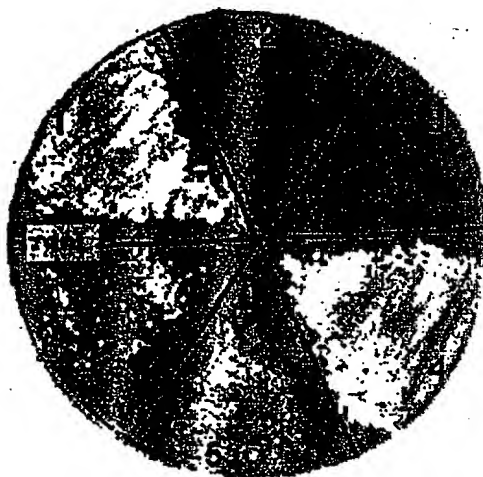




Fig 12 D+E



SD plate without Trp and Leu



SD plate without Trp, Leu, His and Ade

- 1) pGBKT7-53 and pGADT7-T
- 2) pGBKT7-53 and pGAD dna I
- 3) pGBK77ORF104 and pGADT7-T
- 4) pGBKT7-LAM and pCL1
- 5) pGBK77ORF104 and pGAD dna I
- 6) pGBK dna I and pGAD77ORF104

E)

Luminescent 5-Galactosidase Assay

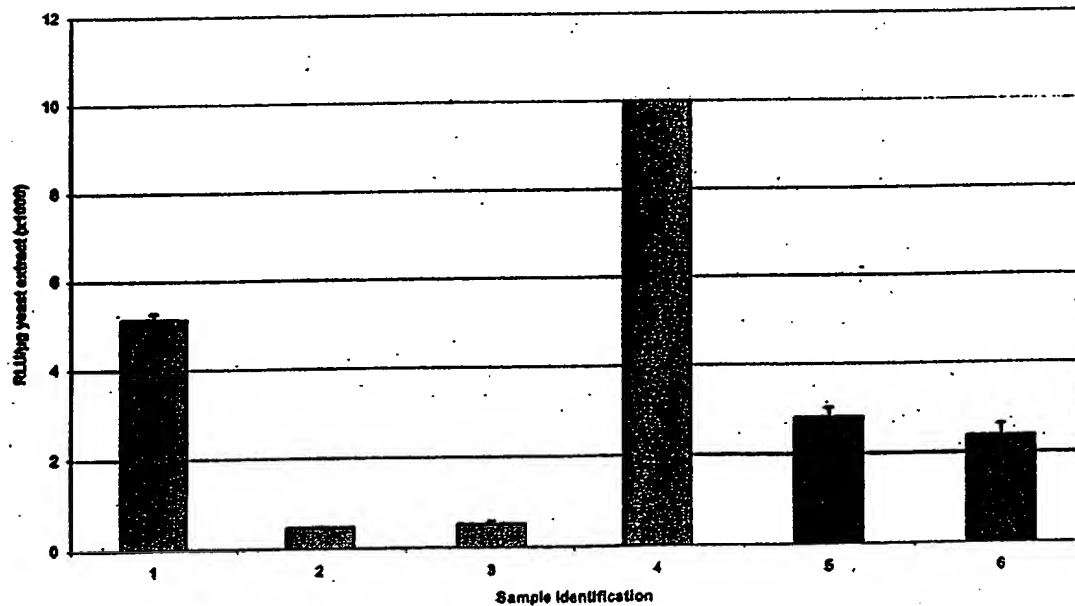
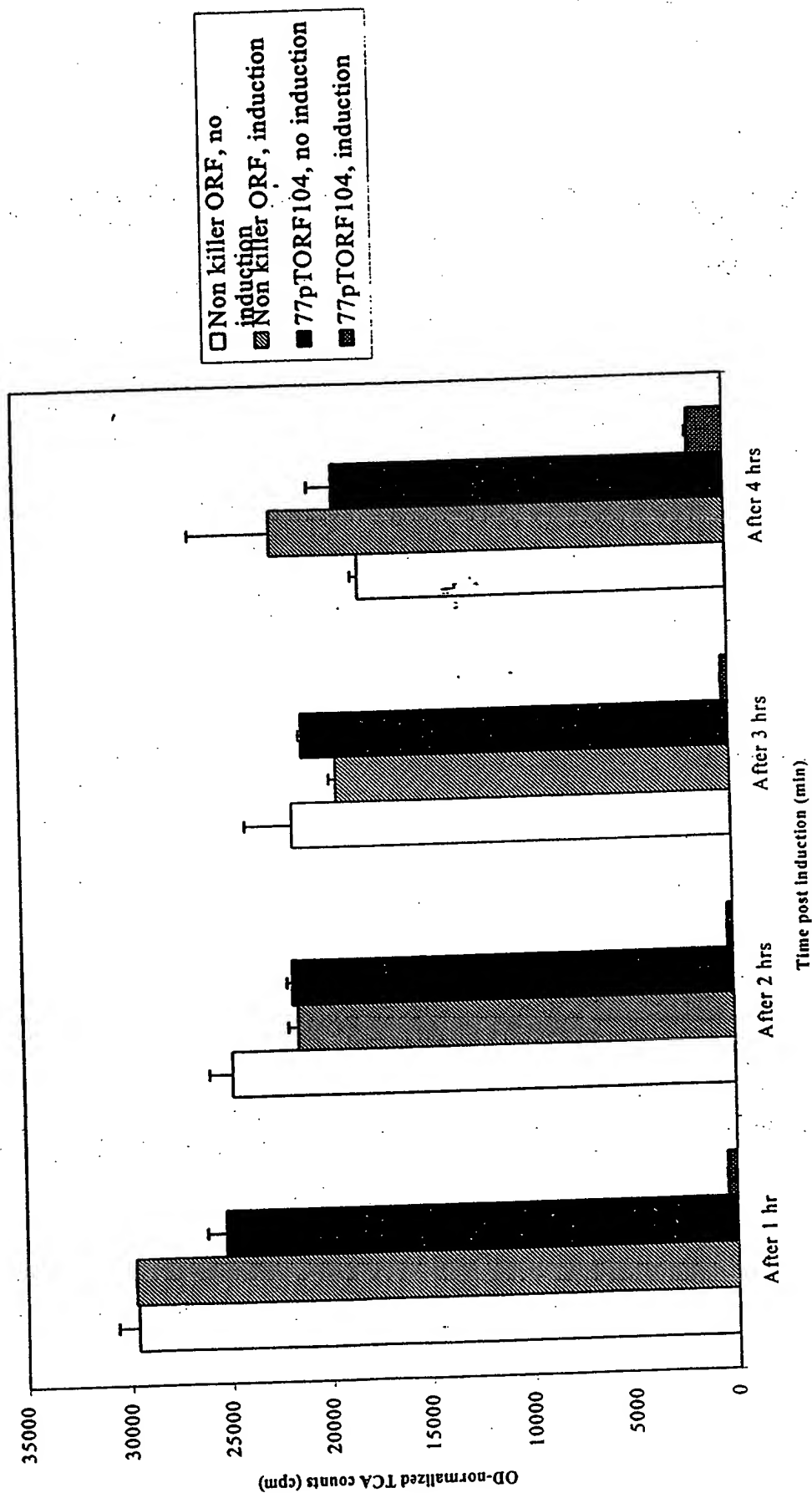


Fig. 13

Effect of 77ORF 104 expression on 3H-Thymidine incorporation



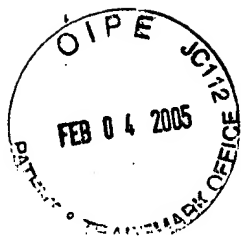
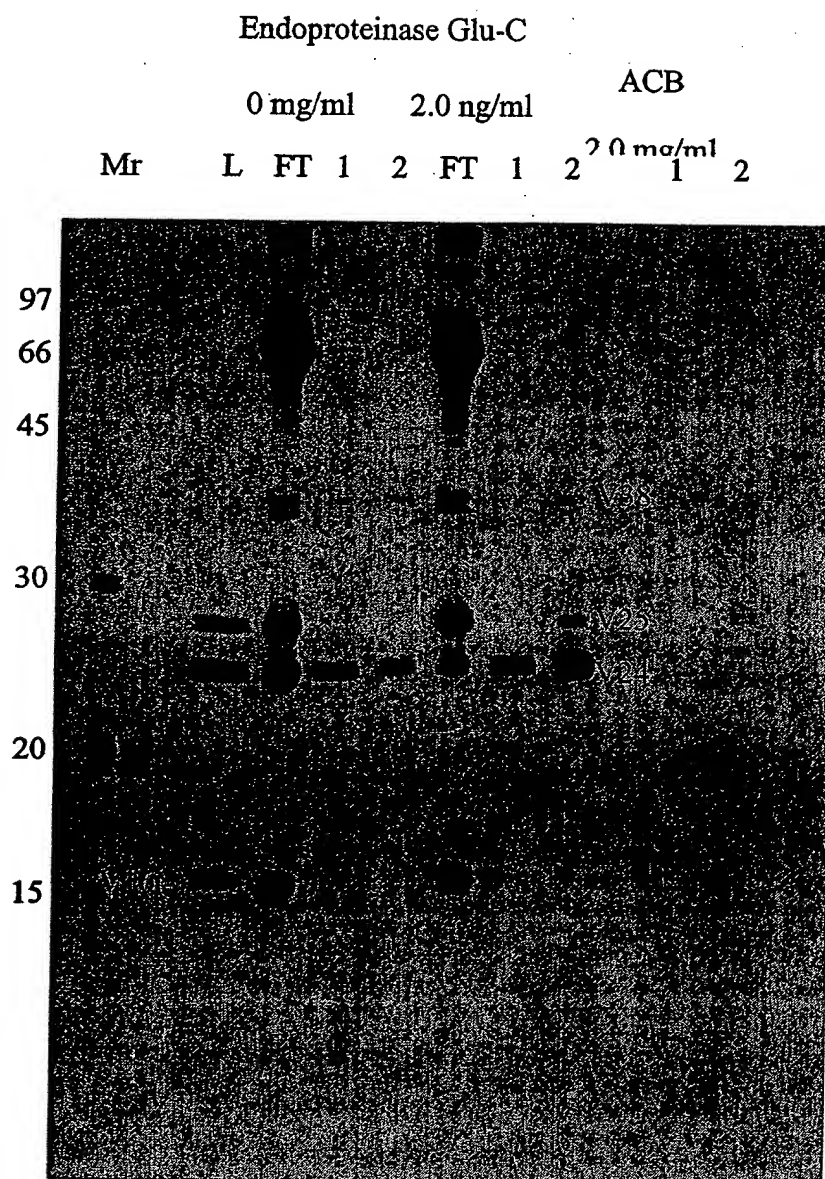


FIGURE 14A



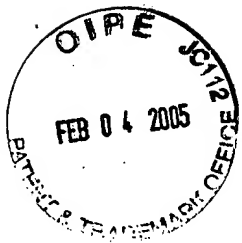
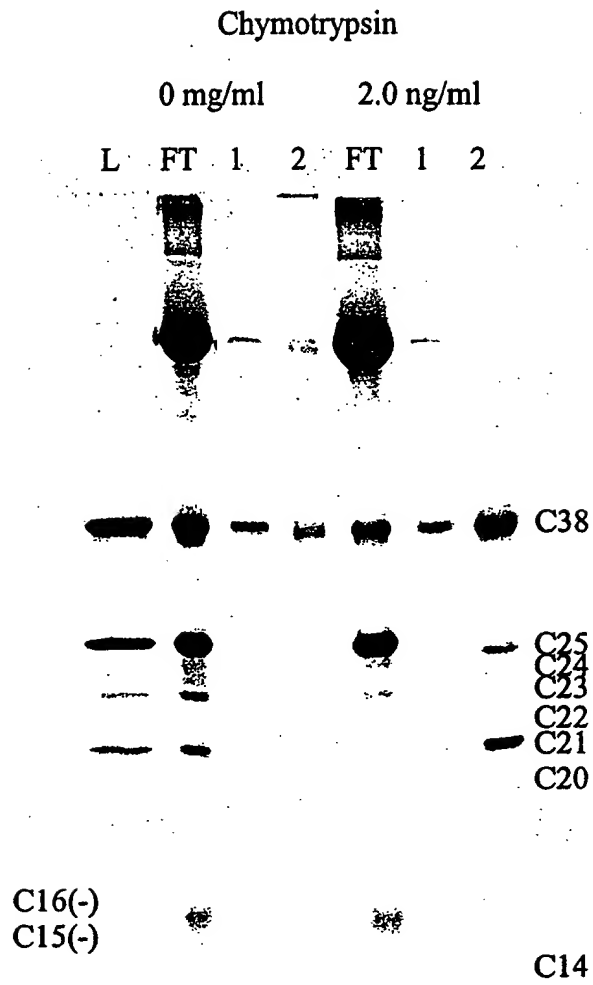


FIGURE 14B





**FIGURE 14C**

Amino acid residues corresponding to interacting partial proteolytic fragments.

Protease	Proteolytic fragment ID (from Fig. 14A, B)	ID of SEQ ID NO: 2 fragment interacting with 77ORF104	
		from amino	to carboxyl
Endoproteinase Glu-C	V24	117	313
	V24	119	313
Chymotrypsin	C38	12	313
	C25	83	313
	C24	77	305
	C23	77	304
	C22	116	313
	C21	131	313
SEQ ID NO: 2	Complete	1	313

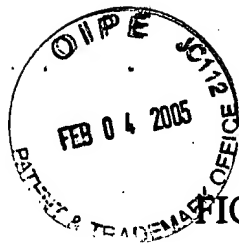


FIGURE 15

SEQ ID NO: 16

>*S.aureus* dnaI : amino acid 150-313

AADDICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTIIYLPFIRTLKG  
GFKDGSFEKKLHRVREANIIMLDDIGAEVTPWVRDEVIGPLLHYRMVHELPTFFSSNFD  
YSELEHHLAMTRDGEKTKAARIIERVKSLSTPYFLSGENFRNN

SEQ ID NO: 17

>*S.aureus* dnaI : nucleotide 448-942

gcagcagatgatatttgtagcaataactaatggggaacaagtgaaggcctttacctt  
tatggtccatttgggacaggtaaatcttttattctaggtgcaattgcgaatcagctcaa  
tctaagaaggtagcttcgacaattatttattaccggaatttattagaacattaaaaggt  
ggctttaagatggttcttttgaaaagaaattacatcgcgtaagagaagcaaacatttta  
atgcttgatgatattggggctgaagaagtgactccatgggtgagagatgaggaattgga  
cctttgctacattatcgaaatggttcatgaattaccaacattctttagttctaattttgac  
tatagtgaattggaacatcatttagcgatgactcgtgatggtgaagagaagactaaagca  
gcacgtattattgaacgtgtcaaactctttgtcaacaccatactttttatcaggagaaaat  
ttcagaaacaattga

SEQ ID NO: 18

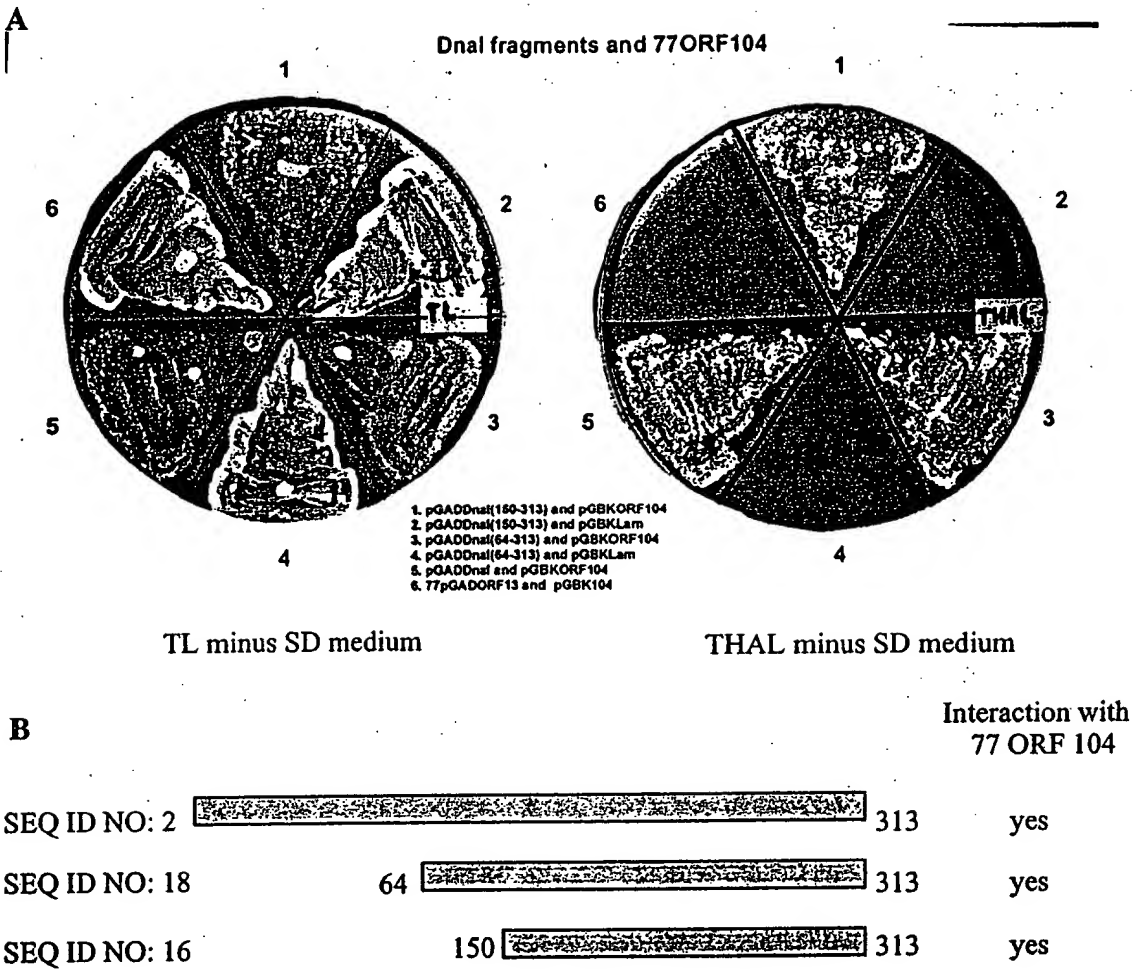
>*S.aureus* dnaI : amino acid 64-313

YKDQQKHVDGHKFADCPNFVKGHVPELYVDNNRIKIRYLQCPCKIKYDEERFEAELITSHH  
MQRDTLNAKLKDIYMNHRDLVDMAADDICTAITNGEQVKGLYLYGPFGTGKSFILGAI  
ANQLKSKKVRSTIIYLPFIRTLKGGFKDGSFEKKLHRVREANIIMLDDIGAEVTPWVR  
DEVIGPLLHYRMVHELPTFFSSNFDYSELEHHLAMTRDGEKTKAARIIERVKSLSTPYF  
LSGENFRNN



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FIGURE 16



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